



OIPE

## RAW SEQUENCE LISTING

DATE: 06/06/2002

PATENT APPLICATION: US/10/017,066A

TIME: 14:37:38

Input Set : D:\51158-20024.txt

Output Set: N:\CRF3\06062002\J017066A.raw

Does Not Comply  
Corrected Diskette Needed

06--> 4 <110> APPLICANT: Arthur B. Raitano  
5 Daniel E.H. Afar  
6 Aya Jakobovits  
7 Mary Faris  
8 Rene S. Hubert  
9 Steve Chappell Mitchell  
10 Douglas C. Saffran  
12 <120> TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR  
13 UP-REGULATED IN PROSTATE CANCER AND USES THEREOF  
16 <130> FILE REFERENCE: 511582002410  
18 <140> CURRENT APPLICATION NUMBER: US 10/017,066A  
19 <141> CURRENT FILING DATE: 2002-05-28  
21 <150> PRIOR APPLICATION NUMBER: US 09/680,728  
W--> 22 <150> PRIOR APPLICATION NUMBER: 2000-10-05  
W--> 24 <150> PRIOR APPLICATION NUMBER: 60/157,902  
25 <151> PRIOR FILING DATE: 1999-10-05  
27 <160> NUMBER OF SEQ ID NOS: 50  
29 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
31 <210> SEQ ID NO: 1  
32 <211> LENGTH: 3136  
33 <212> TYPE: DNA  
34 <213> ORGANISM: Homo Sapiens  
36 <220> FEATURE:  
37 <221> NAME/KEY: CDS  
38 <222> LOCATION: (133)...(1083)  
40 <400> SEQUENCE: 1  
41 cagagaggct gtatttcagt gcagcctgcc agacctcttc tggaggaaga ctggacaaaag 60  
42 ggggtcacac attccttcca tacggttgag cctctacctg cctggtgctg gtcacagttc 120  
43 agctttcttca tg atg gtg gat ccc aat ggc aat gaa tcc agt gct aca tac 171  
44 Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr  
45 1 5 10  
47 ttc atc cta ata ggc ctc cct ggt tta gaa gag gct cag ttc tgg ttg 219  
48 Phe Ile Leu Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu  
49 15 20 25  
51 gcc ttc cca ttg tgc tcc ctc tac ctt att gct gtg cta ggt aac ttg 267  
52 Ala Phe Pro Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu  
53 30 35 40 45  
55 aca atc atc tac att gtg cgg act gag cac agc ctg cat gag ccc atg 315  
56 Thr Ile Ile Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met  
57 50 55 60  
59 tat ata ttt ctt tgc atg ctt tca ggc att gac atc ctc atc tcc acc 363  
60 Tyr Ile Phe Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr  
61 65 70 75

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63	tca tcc atg ccc aaa atg ctg gcc atc ttc tgg ttc aat tcc act acc	411
64	Ser Ser Met Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr	
65	80 85 90	
67	atc cag ttt gat gct tgt ctg cta cag att ttt gcc atc cac tcc tta	459
68	Ile Gln Phe Asp Ala Cys Leu Leu Gln Ile Phe Ala Ile His Ser Leu	
69	95 100 105	
71	tct ggc atg gaa tcc aca gtg ctg ctg gcc atg gct ttt gac cgc tat	507
72	Ser Gly Met Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr	
73	110 115 120 125	
75	gtg gcc atc tgt cac cca ctg cgc cat gcc aca gta ctt acg ttg cct	555
76	Val Ala Ile Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro	
77	130 135 140	
79	cgt gtc acc aaa att ggt gtg gct gct gtg gtg cgg ggg gct gca ctg	603
80	Arg Val Thr Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu	
81	145 150 155	
83	atg gca ccc ctt cct gtc ttc atc aag cag ctg ccc ttc tgc cgc tcc	651
84	Met Ala Pro Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser	
85	160 165 170	
87	aat atc ctt tcc cat tcc tac tgc cta cac caa gat gtc atg aag ctg	699
88	Asn Ile Leu Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu	
89	175 180 185	
91	gcc tgt gat gat atc cgg gtc aat gtc gtc tat ggc ctt atc gtc atc	747
92	Ala Cys Asp Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile	
93	190 195 200 205	
95	atc tcc gcc att ggc ctg gac tca ctt ctc atc tcc ttc tca tat ctg	795
96	Ile Ser Ala Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu	
97	210 215 220	
99	ctt att ctt aag act gtg ttg ggc ttg aca cgt gaa gcc cag gcc aag	843
100	Leu Ile Leu Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys	
101	225 230 235	
103	gca ttt ggc act tgc gtc tct cat gtg tgt gct gtg ttc ata ttc tat	891
104	Ala Phe Gly Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr	
105	240 245 250	
107	gta cct ttc att gga ttg tcc atg gtg cat cgc ttt agc aag cgg cgt	939
108	Val Pro Phe Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg	
109	255 260 265	
111	gac tct ccg ctg ccc gtc atc ttg gcc aat atc tat ctg ctg gtt cct	987
112	Asp Ser Pro Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro	
113	270 275 280 285	
115	cct gtg ctc aac cca att gtc tat gga gtg aag aca aag gag att cga	1035
116	Pro Val Leu Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg	
117	290 295 300	
119	cag cgc atc ctt cga ctt ttc cat gtg gcc aca cac gct tca gag ccc	1083
120	Gln Arg Ile Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro	
121	305 310 315	
123	taggtgtcag tgatcaaact tcttttccat tcagagtcct ctgattcaga ttttaatgtt	1143
124	aacatttttg aagacagtat tcagaaaaaa aatttcctta ataaaaaata caactcagat	1203
125	ccttcaaata tgaaactggt tggggaatct ccattttttc aatattatit tcttctttgt	1263
126	tttcttgcta catataatta ttaataccct gactaggttg tggttgagg gttattactt	1323

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127 ttcatTTTTac catgcagTcc aaatctaaac tgcttctact gatggTTTTac agcatttctga 1383
128 gataagaatg gtacatctag agaacatttg ccaaaggcct aagcacggca aaggaaaata 1443
129 aacacagaat ataataaaat gagataatct agcttaaaac tataacttcc tcttcagaac 1503
130 tccaaccac attggatctc agaaaaatgc tgtcttcaaa atgacttcta cagagaagaa 1563
131 ataatttttc ctctggacac tagcacttaa ggggaagatt ggaagtaaag ccttgaaaag 1623
132 agtacattta cctacgttaa tgaaagtTga cacactgttc tgagagtTtt cacagcatat 1683
133 ggaccctgtt ttctctattt aattttctta tcaacccttt aattaggcaa agatattatt 1743
134 agtaccctca ttgtagccat gggaaaattg atgttcagtg gggatcagtg aattaaatgg 1803
135 ggtcatacaa gtataaaat taaaaaaaaa aaagacttca tgcccaatct catatgatgt 1863
136 ggaagaactg ttagagagac caacagggtg gtgggttaga gatttcaga gtcttacatt 1923
137 ttctagagga ggtatttaat ttcttctcac tcatccagtg ttgtatttag gaatttctctg 1983
138 gcaacagaac tcatggcttt aatcccacta gctattgctt attgtctctg tccaattgcc 2043
139 aattacctgt gtcttggaag aagtgtattc taggttcacc attatggaag attcttatct 2103
140 agaaagtctg catagggtct atagcaagtt atttattttt aaaagttcca taggtgatct 2163
141 tgataggcag tgagggttag gagccaccag ttatgatggg aagtatggaa tggcaggtct 2223
142 tgaagataac attggccttt tgagtgtgac tcgtagctgg aaagtgaggg aatcttcagg 2283
143 accatgcttt atttggggct ttgtgcagta tggaacaggg actttgagac caggaaagca 2343
144 atctgactta ggcattggaa tcaggcattt ttgcttctga ggggctatta ccaagggtta 2403
145 ataggtttca tcttcaacag gatatgacaa cagtgttaac caagaaactc aaattacaaa 2463
146 tactaaaaca tgtgatcata tatgtggtaa gtttcatttt ctttttcaat cctcaggttc 2523
147 cctgatatgg attcctataa catgctttca tccccttttg taatggatat catatttgga 2583
148 aatgcctatt taatacttgt atttgcTgt ggactgtaag cccatgaggg cactgtttat 2643
149 tattgaatgt catctctgtt catcattgac tgctctttgc tcatcattga atccccagc 2703
150 aaagtgccta gaacataaca gtgcttatgc ttgacaccgg ttatttttca tcaaacctga 2763
151 ttcttctgt cctgaacaca tagccaggca attttccagc cttctttgag ttgggtatta 2823
152 ttaaattctg gccattactt ccaatgtgag tggaagtgac atgtgcaatt tctatacctg 2883
153 gctcataaaa cctcccatg tgcagccttt catgttgaca ttaaagtga cttgggaagc 2943
154 tatgtgttac acagagtaaa tcaccagaag cctggatttc tgaaaaaact gtgcagagcc 3003
155 aaacctctgt catttgcaac tcccacttgt atttgtacga ggcagttgga taagtgaaaa 3063
156 ataaagtact attgtgtcaa gaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 3123
157 aaaaaaaaaa aaa 3136

```

159 &lt;210&gt; SEQ ID NO: 2

160 &lt;211&gt; LENGTH: 317

161 &lt;212&gt; TYPE: PRT

162 &lt;213&gt; ORGANISM: Homo Sapiens

164 &lt;400&gt; SEQUENCE: 2

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165 Met Val Asp Pro Asn Gly Asn Glu Ser Ser Ala Thr Tyr Phe Ile Leu
166 1 5 10 15
167 Ile Gly Leu Pro Gly Leu Glu Glu Ala Gln Phe Trp Leu Ala Phe Pro
168 20 25 30
169 Leu Cys Ser Leu Tyr Leu Ile Ala Val Leu Gly Asn Leu Thr Ile Ile
170 35 40 45
171 Tyr Ile Val Arg Thr Glu His Ser Leu His Glu Pro Met Tyr Ile Phe
172 50 55 60
173 Leu Cys Met Leu Ser Gly Ile Asp Ile Leu Ile Ser Thr Ser Ser Met
174 65 70 75 80
175 Pro Lys Met Leu Ala Ile Phe Trp Phe Asn Ser Thr Thr Ile Gln Phe
176 85 90 95
177 Asp Ala Cys Leu Leu Gln Ile Phe Ala Ile His Ser Leu Ser Gly Met

```

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```

178          100          105          110
179 Glu Ser Thr Val Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile
180          115          120          125
181 Cys His Pro Leu Arg His Ala Thr Val Leu Thr Leu Pro Arg Val Thr
182          130          135          140
183 Lys Ile Gly Val Ala Ala Val Val Arg Gly Ala Ala Leu Met Ala Pro
184 145          150          155          160
185 Leu Pro Val Phe Ile Lys Gln Leu Pro Phe Cys Arg Ser Asn Ile Leu
186          165          170          175
187 Ser His Ser Tyr Cys Leu His Gln Asp Val Met Lys Leu Ala Cys Asp
188          180          185          190
189 Asp Ile Arg Val Asn Val Val Tyr Gly Leu Ile Val Ile Ile Ser Ala
190          195          200          205
191 Ile Gly Leu Asp Ser Leu Leu Ile Ser Phe Ser Tyr Leu Leu Ile Leu
192          210          215          220
193 Lys Thr Val Leu Gly Leu Thr Arg Glu Ala Gln Ala Lys Ala Phe Gly
194 225          230          235          240
195 Thr Cys Val Ser His Val Cys Ala Val Phe Ile Phe Tyr Val Pro Phe
196          245          250          255
197 Ile Gly Leu Ser Met Val His Arg Phe Ser Lys Arg Arg Asp Ser Pro
198          260          265          270
199 Leu Pro Val Ile Leu Ala Asn Ile Tyr Leu Leu Val Pro Pro Val Leu
200          275          280          285
201 Asn Pro Ile Val Tyr Gly Val Lys Thr Lys Glu Ile Arg Gln Arg Ile
202          290          295          300
203 Leu Arg Leu Phe His Val Ala Thr His Ala Ser Glu Pro
204 305          310          315
206 <210> SEQ ID NO: 3
207 <211> LENGTH: 320
208 <212> TYPE: PRT
209 <213> ORGANISM: Rat Protein
211 <400> SEQUENCE: 3
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213 1          5          10          15
214 Pro Gly Leu Glu Glu Ala His Phe Trp Phe Gly Phe Pro Leu Leu Ser
215          20          25          30
216 Met Tyr Ala Val Ala Leu Phe Gly Asn Cys Ile Val Val Phe Ile Val
217          35          40          45
218 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
219          50          55          60
220 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
221 65          70          75          80
222 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Thr Phe Asp Ala Cys
223          85          90          95
224 Leu Ala Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
225          100          105          110
226 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
227          115          120          125
228 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Val Gln Ile Gly

```

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```

229      130      135      140
230 Met Val Ala Leu Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
231 145      150      155      160
232 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser
233      165      170      175
234 Tyr Cys Val His Gln Asp Val Met Lys Leu Ala Tyr Thr Asp Thr Leu
235      180      185      190
236 Pro Asn Val Val Tyr Gly Leu Thr Ala Ile Leu Leu Val Met Gly Val
237      195      200      205
238 Asp Val Met Phe Ile Ser Leu Ser Tyr Phe Leu Ile Ile Arg Ala Val
239      210      215      220
240 Leu Gln Leu Pro Ser Lys Ser Glu Arg Ala Lys Ala Phe Gly Thr Cys
241 225      230      235      240
242 Val Ser His Ile Gly Val Val Leu Ala Phe Tyr Val Pro Leu Ile Gly
243      245      250      255
244 Leu Ser Val Val His Arg Phe Gly Asn Ser Leu Asp Pro Ile Val His
245      260      265      270
246 Val Leu Met Gly Asp Val Tyr Leu Leu Leu Pro Pro Val Ile Asn Pro
247      275      280      285
248 Ile Ile Tyr Gly Ala Lys Thr Lys Gln Ile Arg Thr Arg Val Leu Ala
249      290      295      300
250 Met Phe Lys Ile Ser Cys Asp Lys Asp Ile Glu Ala Gly Gly Asn Thr
251 305      310      315      320
253 <210> SEQ ID NO: 4
254 <211> LENGTH: 320
255 <212> TYPE: PRT
256 <213> ORGANISM: Homo Sapiens
258 <400> SEQUENCE: 4
259 Met Ser Ser Cys Asn Phe Thr His Ala Thr Cys Val Leu Ile Gly Ile
260 1      5      10      15
261 Pro Gly Leu Glu Lys Ala His Phe Trp Val Gly Phe Pro Leu Leu Ser
262      20      25      30
263 Met Tyr Val Val Ala Met Cys Gly Asn Cys Ile Val Val Phe Ile Val
264      35      40      45
265 Arg Thr Glu Arg Ser Leu His Ala Pro Met Tyr Leu Phe Leu Cys Met
266      50      55      60
267 Leu Ala Ala Ile Asp Leu Ala Leu Ser Thr Ser Thr Met Pro Lys Ile
268 65      70      75      80
269 Leu Ala Leu Phe Trp Phe Asp Ser Arg Glu Ile Ser Ile Glu Ala Cys
270      85      90      95
271 Leu Thr Gln Met Phe Phe Ile His Ala Leu Ser Ala Ile Glu Ser Thr
272      100      105      110
273 Ile Leu Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys His Pro
274      115      120      125
275 Leu Arg His Ala Ala Val Leu Asn Asn Thr Val Thr Ala Gln Ile Gly
276      130      135      140
277 Ile Val Ala Val Val Arg Gly Ser Leu Phe Phe Phe Pro Leu Pro Leu
278 145      150      155      160
279 Leu Ile Lys Arg Leu Ala Phe Cys His Ser Asn Val Leu Ser His Ser

```

RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:41; N Pos. 6,12,15  
Seq#:42; N Pos. 3,6,12,15  
Seq#:43; N Pos. 12,15  
Seq#:44; N Pos. 3,12,15  
Seq#:45; N Pos. 3,9,18  
Seq#:46; N Pos. 3,9  
Seq#:47; N Pos. 6,9,21  
Seq#:48; N Pos. 1,13,16  
Seq#:49; N Pos. 1,7,10,16  
Seq#:50; N Pos. 10,16,19